

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,277
Source: 1 FWP
Date Processed by STIC: 1/20/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/20/2006

PATENT APPLICATION: US/10/564,277

TIME: 12:11:10

Input Set : N:\SMITH\PTO.TAS19.txt

Output Set: N:\CRF4\01202006\J564277.raw

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3 <110> APPLICANT: Develogen Aktiengesellschaft fur entwicklungsbiolo
5 <120> TITLE OF INVENTION: Use of DG153 or DG177 secreted protein products for
6     preventing and treating pancreatic diseases and/or
7     obesity and/or metabolic syndrome
9 <130> FILE REFERENCE: 31130PWO WWHC
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/564,277
C--> 12 <141> CURRENT FILING DATE: 2006-01-11
14 <150> PRIOR APPLICATION NUMBER: EP03015883.6
15 <151> PRIOR FILING DATE: 2003-07-11
17 <150> PRIOR APPLICATION NUMBER: EP03016710.0
18 <151> PRIOR FILING DATE: 2003-07-22
20 <160> NUMBER OF SEQ ID NOS: 11
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1103
26 <212> TYPE: DNA
27 <213> ORGANISM: human
29 <220> FEATURE:
30 <223> OTHER INFORMATION: nucleotide sequence of human DG153 protein
32 <400> SEQUENCE: 1
33 cttcgggtcct gctgtagtgc cttctgcgcc aggcccggtt caatcagcgg ccacaactgt 60
34 ctagggctca gacaccacca gccaatgagg gagggcacgt ggagcccgct ctgggctcgc 120
35 ggctcctgac caatggggaa gtggcatgtg ggagggcgcc ggggttcccc ccgccaatgg 180
36 ggagctacgg cgcgcggccg ggacttggag gcggtgcggc gcggcggggtg cggttcagtc 240
37 ggtcggcggc ggcagcggag gaggaggagg aggaggagga tgaggaggat gaggaggatg 300
38 tgggcccacgc aggggctggc ggtgcgcgtg gctctgagcg tgctgccggg cagccgggcg 360
39 ctgcggccgg gcgactgcga agtttgatt tcttatctgg gaagatttta ccaggacctc 420
40 aaagacagag atgtcacatt ctcaccagcc actattgaaa acgaacttat aaagttctgc 480
41 cgggaagcaa gaggcaaaga gaatcggttg tgctactata tcggggccac agatgatgca 540
42 gccacaaaaa tcatcaatga ggtatcaaag cctctggccc accacatccc tgtggagaag 600
43 atctgtgaga agcttaagaa gaaggacagc cagatatgtg agcttaagta tgacaagcag 660
44 atcgacctga gcacagtga cctgaagaag ctccgagtta aagagctgaa gaagattctg 720
45 gatgactggg gggagacatg caaaggctgt gcagaaaagt ctgactacat ccggaagata 780
46 aatgaactga tgcctaaata tgcccccaag gcagccagtg caccgaccga ttgtagtct 840
47 gctcaatctc tgttgcacct gaggggggaaa aaacagttca actgcttact cccaaaacag 900
48 cctttttgta atttattttt taagtgggct cctgacaata ctgtatcaga tgtgaagcct 960
49 ggagctttcc tgatgatgct ggccctacag taccctcatg aggggattcc cttccttctg 1020
50 ttgctggtgt actctaggac ttcaaagtgt gtctgggatt tttttattaa agaaaaaaaa 1080
51 tttctagctg tcaaaaaaaaa aaa 1103
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 234
56 <212> TYPE: PRT
57 <213> ORGANISM: human

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59 <220> FEATURE:

60 <223> OTHER INFORMATION: amino acid sequence of human DG153 protein, longer
61 variant

63 <400> SEQUENCE: 2

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64 Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro Arg Gln Trp
65   1           5           10           15
67 Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg Arg Gly Gly
68           20           25           30
70 Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg Arg
71           35           40           45
73 Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val
74           50           55           60
76 Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly
77  65           70           75           80
79 Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu
80           85           90           95
82 Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu
83           100          105          110
85 Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr
86           115          120          125
88 Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val
89           130          135          140
91 Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys
92 145           150           155           160
94 Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln
95           165           170           175
97 Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu
98           180          185          190
100 Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu
101           195          200          205
103 Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala
104           210          215          220
106 Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu
107 225          230

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111 <210> SEQ ID NO: 3

112 <211> LENGTH: 179

113 <212> TYPE: PRT

114 <213> ORGANISM: human

116 <220> FEATURE:

117 <223> OTHER INFORMATION: amino acid sequence of human DG153 protein,
118 shorter variant

120 <400> SEQUENCE: 3

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121 Met Trp Ala Thr Gln Gly Leu Ala Val Ala Leu Ala Leu Ser Val Leu
122   1           5           10           15
124 Pro Gly Ser Arg Ala Leu Arg Pro Gly Asp Cys Glu Val Cys Ile Ser
125           20           25           30
127 Tyr Leu Gly Arg Phe Tyr Gln Asp Leu Lys Asp Arg Asp Val Thr Phe
128           35           40           45
130 Ser Pro Ala Thr Ile Glu Asn Glu Leu Ile Lys Phe Cys Arg Glu Ala

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131      50      55      60
133 Arg Gly Lys Glu Asn Arg Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp
134 65      70      75      80
136 Ala Ala Thr Lys Ile Ile Asn Glu Val Ser Lys Pro Leu Ala His His
137      85      90      95
139 Ile Pro Val Glu Lys Ile Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln
140      100      105      110
142 Ile Cys Glu Leu Lys Tyr Asp Lys Gln Ile Asp Leu Ser Thr Val Asp
143      115      120      125
145 Leu Lys Lys Leu Arg Val Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp
146      130      135      140
148 Gly Glu Thr Cys Lys Gly Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys
149 145      150      155      160
151 Ile Asn Glu Leu Met Pro Lys Tyr Ala Pro Lys Ala Ala Ser Ala Arg
152      165      170      175
154 Thr Asp Leu
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 3714
161 <212> TYPE: DNA
162 <213> ORGANISM: human
164 <220> FEATURE:
165 <223> OTHER INFORMATION: nucleotide sequence of human DG177 protein
167 <400> SEQUENCE: 4
168 ggcacgaggg atcggcggag ctccacctc cgcttacagc tcgctgccgc cgtcctgccc 60
169 cgcgcccca ggagacctg accagaccac gatgtggaaa cgctggctcg cgctcgcgct 120
170 cgcgctggtg gcggtcgctt ggggtccgcgc cgaggaagag ctaaggagca aatccaagat 180
171 ctgtgccaat gtgttttgtg gagccggccg ggaatgtgca gtcacagaga aaggggaacc 240
172 cacctgtctc tgcattgagc aatgcaaac tcacaagagg cctgtgtgtg gcagtaatgg 300
173 caagacctac ctcaaccact gtgaactgca tcgagatgcc tgcctcactg gatccaaaat 360
174 ccaggttgat tacgatggac actgcaaga gaagaaatcc gtaagtccat ctgccagccc 420
175 agttgtttgc tatcagtcca accgtgatga gtcctgcacg cgcatcatcc agtggctgga 480
176 agctgagatc attccagatg gctggttctc taaaggcagc aactacagtg aaatcctaga 540
177 caagtatttt aagaactttg ataatggtga ttctcgctcg gactccagtg aattcctgaa 600
178 gtttgtggaa cagaatgaaa ctgccatcaa tattacaacg tatccagacc aggagaacaa 660
179 caagttgctt aggggactct gtgttgatgc tctcattgaa ctgtctgatg aaaatgctga 720
180 ttggaaactc agcttccaag agtttctcaa gtgcctcaac ccatctttca accctcctga 780
181 gaagaagtgt gccctggagg atgaaacgta tgcagatgga gctgagaccg aggtggactg 840
182 taaccgctgt gtctgtgcct gtggaaattg ggtctgtaca gccatgacct gtgacggaaa 900
183 gaatcagaag ggggcccaga ccagacaga ggaggagatg accagatatg tccaggagct 960
184 ccaaaagcat caggaaacag ctgaaaagac caagagagtg agcaccaaag agatctaata 1020
185 aggaggcaca gaccagtgtc tggatcccag catcttctcc acttcagcgc tgagttcagt 1080
186 atacacaagt gtctgtctca gtcgccaaat caccagtatt tgcttatata gcaatgagtt 1140
187 ttattttgtt tatttgtttt gcaataaagg atatgaaggg ggctggctag gaaggggaagg 1200
188 gccacagcct tcatctctag gagtgcttta agagaaactg taaatgggtg tctggggctg 1260
189 gaggctagta aggaaactgc atcacgattg aaagaggaac agacccaaat ctgaacctct 1320
190 tttgagttta ctgcatctgt cagcaggctg cagggagtgc acacgatgcc agagagaact 1380
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192 tccagcctct ttccattgcc gtcagcatga cagacctcca gcatccacgc atctcttggt 1500
193 cccaataact gcctctagat acatagccat actgctagtt aaccagtggt ccctcagact 1560

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194 tggatggagt ttctgggagg gtacacccaa atgatgcaga tacttggtata ctttgagccc 1620
195 cttagcgacc taaccaaatt ttaaaaatac tttttaccaa aggtgctatt tctctgtaaa 1680
196 acactttttt tttggcaagt tgactttatt cttcaattat tatcattata ttattgtttt 1740
197 ttaatatattt attttcttga ctaggtatta agcttttgta attatttttc agtagtccca 1800
198 ccacttcata ggtggaagga gtttgggggt cttcctgggt caggggctga aataacccag 1860
199 atgccccac cctgccacat actagatgca gcccatagtt ggcccccta gcttccagca 1920
200 gtccactatc tgccagagga gcaagggtgc cttagaccga agccagggga agaagcatct 1980
201 tcataaaaaa ctttcaagat ccaaacatta atttgttttt atttattctg agaagttgag 2040
202 gcaaatcagt attcccaagg atggcgacaa gggcagccaa gcagggctta ggatatccca 2100
203 gcctaccaat atgctcattc gactaactag gagggtgagt tggccctgtc tcttcttttt 2160
204 tctggacctc agtttcttca gtgagctggg aagaatgcac taaccttttg atttgataag 2220
205 ttataaattc tgtggttctg atcattgggtc cagaggggag atagggttctt gtgattttttc 2280
206 cttcttctct atagaataaa tgaaatcttg ttactagaac aagaaatgtc agatggccaa 2340
207 aaacaagatg accagatttg atctcagcct gatgacccta caggtcgtgc tatgatattg 2400
208 agtcctcatg ggtaaagcag gaagagagtg ggaaagagaa ccacccact ctgtcttcat 2460
209 atttgcatth catgtttaac ctccggctgg aaatagaaag cattccctta gagatgagga 2520
210 taaaagaaag tttcagattc aacaggggga agaaaatgga gatttaatcc taaaactgtg 2580
211 acctggggag gtcagtcatt tacagttagt cctgtgtctt tcgacttctg tgattattaa 2640
212 cccactcac taccctgttt cagatgcatt tggaaatacca aagattaaat ccttgacata 2700
213 agatctcatt tgcagaaagc agattaaaga ccatcagaag gaaattattt aggttgtaat 2760
214 gcacaggcaa ctgtgagaaa ctgttgtgcc aaaaatagaa ttccttctag ttttcttgt 2820
215 tctcatttga aaggagaaaa ttccactttg tttagcattt caagctttta tgtatccatc 2880
216 ccatctaaaa actcttcaaa ctccacttgt tcagtctgaa atgcagctcc ctgtccaagt 2940
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218 tgggaggagg gcaagagtac accaatttgt taaaagcaag aaaccacagt gtctcttcac 3060
219 tagtcattta gaacatgggt atcatccaag actactctac cctgcaacat tgaactccca 3120
220 agagcaaatc cacattcctc ttgagttctg cagcttctgt gtaaataaggg cagctgtcgt 3180
221 ctatgccgta gaatcacatg atctgaggac cattcatgga agctgctaaa tagcctagtc 3240
222 tggggaggtc tccataaagt tttgcatgga gcaacaaac aggattaaac taggtttggt 3300
223 tccttcagcc ctctaaaagc atagggctta gcctgcaggc ttccttgggc tttctctgtg 3360
224 tgtgtagttt tgtaaacact atagcatctg ttaagatcca gtgtccatgg aaacattccc 3420
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226 aagcccacgt ggaccagtct gaatgtcttt cctttacacc tatgttttta agtagtcaaa 3540
227 cttcaagaaa caatctaaac aagtttctgt tgcataatgt tttgtgaact tgtatttgta 3600
228 tttagtaggc ttctatattg catttaactt gtttttgtaa ctctgattc ttccttttctg 3660
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232 <210> SEQ ID NO: 5

233 <211> LENGTH: 308

234 <212> TYPE: PRT

235 <213> ORGANISM: human

237 <220> FEATURE:

238 <223> OTHER INFORMATION: amino acid sequence of human DG177 protein

240 <400> SEQUENCE: 5

241 Met Trp Lys Arg Trp Leu Ala Leu Ala Leu Val Ala Val Ala

242 1 5 10 15

244 Trp Val Arg Ala Glu Glu Glu Leu Arg Ser Lys Ser Lys Ile Cys Ala

245 20 25 30

247 Asn Val Phe Cys Gly Ala Gly Arg Glu Cys Ala Val Thr Glu Lys Gly

248 35 40 45

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250 Glu Pro Thr Cys Leu Cys Ile Glu Gln Cys Lys Pro His Lys Arg Pro
251      50                      55                      60
253 Val Cys Gly Ser Asn Gly Lys Thr Tyr Leu Asn His Cys Glu Leu His
254 65                      70                      75                      80
256 Arg Asp Ala Cys Leu Thr Gly Ser Lys Ile Gln Val Asp Tyr Asp Gly
257                      85                      90                      95
259 His Cys Lys Glu Lys Lys Ser Val Ser Pro Ser Ala Ser Pro Val Val
260                      100                      105                      110
262 Cys Tyr Gln Ser Asn Arg Asp Glu Leu Arg Arg Arg Ile Ile Gln Trp
263                      115                      120                      125
265 Leu Glu Ala Glu Ile Ile Pro Asp Gly Trp Phe Ser Lys Gly Ser Asn
266                      130                      135                      140
268 Tyr Ser Glu Ile Leu Asp Lys Tyr Phe Lys Asn Phe Asp Asn Gly Asp
269 145                      150                      155                      160
271 Ser Arg Leu Asp Ser Ser Glu Phe Leu Lys Phe Val Glu Gln Asn Glu
272                      165                      170                      175
274 Thr Ala Ile Asn Ile Thr Thr Tyr Pro Asp Gln Glu Asn Asn Lys Leu
275                      180                      185                      190
277 Leu Arg Gly Leu Cys Val Asp Ala Leu Ile Glu Leu Ser Asp Glu Asn
278                      195                      200                      205
280 Ala Asp Trp Lys Leu Ser Phe Gln Glu Phe Leu Lys Cys Leu Asn Pro
281                      210                      215                      220
283 Ser Phe Asn Pro Pro Glu Lys Lys Cys Ala Leu Glu Asp Glu Thr Tyr
284 225                      230                      235                      240
286 Ala Asp Gly Ala Glu Thr Glu Val Asp Cys Asn Arg Cys Val Cys Ala
287                      245                      250                      255
289 Cys Gly Asn Trp Val Cys Thr Ala Met Thr Cys Asp Gly Lys Asn Gln
290                      260                      265                      270
292 Lys Gly Ala Gln Thr Gln Thr Glu Glu Glu Met Thr Arg Tyr Val Gln
293                      275                      280                      285
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296                      290                      295                      300
298 Thr Lys Glu Ile
299 305

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303 <210> SEQ ID NO: 6
304 <211> LENGTH: 26
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
311 <220> FEATURE:
312 <223> OTHER INFORMATION: mouse DG153 forward primer
314 <400> SEQUENCE: 6
315 agagaatcgg ttgtgctact acattg
318 <210> SEQ ID NO: 7
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date